

Figure 1
Fatty Acid Biosynthetic Pathway

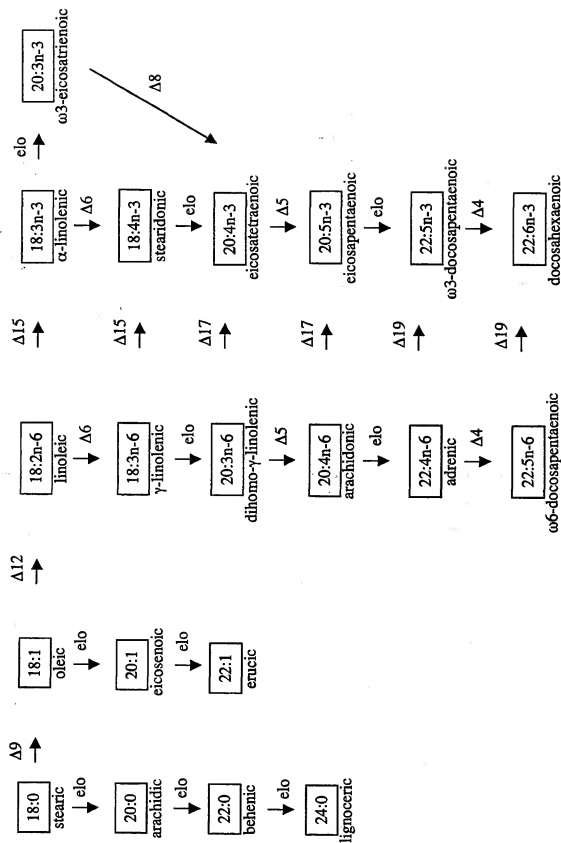


Figure 2

Gene Sequence of *sdd17*, an Omega-3 Fatty Acid Desaturase Gene
from *Saprolegnia diclina* (ATCC 56851)

1 ATGACTGAGG ATAAGACGAA GGTGAGTTC CCGACGCTCA CGGAGCTCAA
51 GCACTCGATC CCGAACGCGT GCTTTGAGTC GAACCTCGGC CTCTCGCTCT
101 ACTACACGGC CCGCGCGATC TTCAACGCGT CGGCCTCGGC GGCCTGCTCT
151 TACGCGGGCG GCTCGACGCC GTTCATTGCC GATAACGTTT TGCTCCACGC
201 GCTCGTTTGC GCCACCTACA TCTACGTGCA GGGCGTCATC TTCTGGGGCT
251 TCTTCACGGT CGGCCACGAC TCGGGCCACT CGGCCTTCTC GCGCTACCAC
301 AGCGTCAACT TTATCATCGG CTGCATCATG CACTCTGCGA TTTTGACGCC
351 GTTCGAGAGC TGGCGCGTGA CGCACCGCCA CCACCACAAG AACACGGGCA
401 ACATTGATAA GGACGAGATC TTTTACCCGC ACCGGTCGGT CAAGGACCTC
451 CAGGACGTGC GCCAATGGGT CTACACGCTC GCGGGTGGCT GGTTTGTCTA
501 CTTGAAGGTC GGGTATGCCC CGCGCACGAT GAGCCACTTT GACCCGTGGG
551 ACCCGCTCCT CCTTCGCCGC GCGTCGGCCG TCATCGTGTC GCTCGGCGTC
601 TGGGCGCCT TCTTCGCCGC GTACGCGTAC CTCACATACT CGCTCGGCTT
651 TGCGGTCATG GGCTCTACT ACTATGCGCC GCTCTTGTGC TTTGCTTCGT
701 TCCTCGTCAT TACGACCTTC TTGCACCACA ACGACGAAGC GACCCGTGG
751 TACGGCGACT CGGAGTGGAC GTACGTCAAG GGCACCTCT CGAGCGTCGA
801 CCGTCTGTAC GCGCGGTTTC TGGACAACCT GAGCCACCAC ATTGGCACGC
851 ACCAGGTCCA CCACCTGTTC CCGATCATTC CGCACTACAA GCTCAACGAA
901 GCCACCAAGC ACTTTGCGGC CGCGTACCCG CACCTCGTGC GCAGGAACGA
951 CGAGCCCATC ATCAGCGCCT TCTTCAAGAC CGCGCACCTC TTTGTCAACT
1001 ACGGCGCTGT GCCCGAGACG GCGCAGATCT TCACGCTCAA AGAGTCGGCC
1051 GCGGCCGCCA AGGCCAAGTC GGACTAA

CGGAGCTCAA

Figure 3

Amino Acid Sequence of an Omega-3 Fatty Acid Desaturase (SDD17) from *Saprolegnia diclina* (ATCC 56851)

1 MTEDKTKVEF PTLTELKHSI PNACFESNLG LSLYYTARAI FNASASAALL
51 YAARSTPFIA DNVLLHALVC ATYIYVQGVF FWGFFTVGHD CGHSAFSRYH
101 SVNFIIGCIM HSAILTPFES WRVTHRHHHK NTGNIDKDEI FYPHRSVKDL
151 QDVRQWVYTL GGAWFVYLKV GYAPRTMSHF DPWDPLLLRR ASAVIVSLGV
201 WAAFFAAYAY LTYSLGFAVM GLYYYAPLFV FASFLVITTF LHHNDEATPW
251 YGDSEWTYVK GNLSSVDRSY GAFVDNLSSH IGHQVHHLF PIIPHYKLNE
301 ATKHFAAAYP HLVRNDEPI ITAFFKTAHL FVNYGAVPET AQIFTLKESA
351 AAKAKSD*

Figure 4

Comparative analysis of *S. diclina* Delta 17-desaturase (SDD17.pep)
& *Synechocystis* sp. Delta 15-desaturase (SYCDESB)

Frame: 2 initn: 733 initl: 305 opt: 689 Z-score: 996.8 expect(): 1.5e-47
40.9% identity in 269 aa overlap
(76-336:204-471)

	50	60	70	80	90	100
SDD17.pep	SAALLVAARSTPF	FIADNVLLHALVCATY	TVVQGVLF	WGFFTVGH	DGHSAPSRYSVNFI	
SYCDESB	YFFLDVGLIAGFY	ALAAAYLD	SWFFYP	IFVLIQ	GLFWLSLFV	VGHDCGHSKSPKSTLNW
	530	560	590	620	650	680
	110	120	130	140	150	160
SDD17.pep	IGCIMHSAILTP	FESWRVTRH	HHKNTGNID	KDEIFYP	HRSVKDLQ	DVRQWVYITLG
SYCDESB	IGHLSHTPI	LVPYHGWRL	SHRTHHANT	GNIDTDES	WYPVSE	QKYNQMAWYEKLLRFYFL
	710	740	770	800	830	860
	170	180	190	200	210	220
SDD17.pep	GANFVYLK	VGYAPRIMSH	FDPDW	PILLRRAS	AVISLGV	WAFFAAYAL
SYCDESB	IAYPIYL	FRSPNRQ	SHFM	PGSPLFR	PCKEAA	VLTSTFALAA
	890	920	950	980	1010	1040
	230	240	250	260	270	280
SDD17.pep	GLVYYAPLE	VFAFLVIT	ITFLHHN	DEATPWY	GDSEWTV	KGNLSSVDRSYGAFV
SYCDESB	LKFTYAP	YLVFVW	LDLVIT	LHHTED	NIPWYRG	DDWYFLK
	1070	1100	1130	1160	1190	1220
	290	300	310	320	330	
SDD17.pep	IGTHQVHH	LFPIIPHY	KINEATK	HFAPAA	YPHLVRR	NDEPITTAFFKT
SYCDESB	IGTHVAH	HIFSNM	PHYKLR	RATEAT	KPILGE	YRYSD
	1250	1280	1310	1340	1370	1400
	340	350				
SDD17.pep	PETAQIF	ITLKES	AAAAAK	KASD		
SYCDESB	VYYQSP	SNNGYQ	KPKL	ILILIES	NQHR	EGROYVM
	1430	1460	1490	1520	1550	1580

Figure 5

Comparative analysis of *S. diclina* Delta 17-desaturase (SDD17.pep)
C. elegans Delta 17-desaturase (CELEFAT)

Frame: 1 initn: 490 initl: 222 opt: 502 Z-score: 724.0 expect(): 2.3e-32
 31.6% identity in 310 aa overlap
 (2-303:49-347)

					10	20	30
SDD17.pep					MTEDKTKVEFPITLTELKHSIPNACFESNLGL		
CELEFAT	VTGGDVLVDARASLEEKEAPRDVNANTKQATTEEPRIQLPTVDAFRRAIPAHCFERDLVK	80	110	140	170	200	230
		40	50	60	70	80	90
SDD17.pep	SLYYTARAIFNASASAAALLYAARSTFFTADNVLIHALVCATYIYVGVIWFPGFTVGHDC						
CELEFAT	SIRYLVDQF-----AALTILYFALPAFETPGLFGLYLVNIFM-----GVFGFALFVVGHDC	260	290	320	350	380	
		100	110	120	130	140	
SDD17.pep	GHSAPSRYSYHVNFIIGCTMHSAILTPFESWRVIRHHHKVITGNIDK-----EIFYPHRSVKD						
CELEFAT	LHGSFSDNQNLNDFIGHIAFSPLSPYPYFPAQKSKHLHAFINHIKDKHGHVWIQDKOWEA	410	440	470	500	530	560
		150	160	170	180	190	200
SDD17.pep	LQDVRCQW-----YTLGGAWF-VYLKVGYPRTIMSHFDPWDPLILRRASAVIVSLGVWAAF						
CELEFAT	MPSWKWENFIPFSGWIKWFPVYTLGFC-----DGSHFWPYSSLFVRNSDRVQCVISGICCC	590	620	650	680	710	740
		210	220	230	240	250	260
SDD17.pep	FAAYAYLTYSLGFAVMGLYYAPLFVFASFVLTITFTFLHHNEATPWIQDSEWTVKGNLS						
CELEFAT	VCAYIALTIAGSYSNWFYVWVPLSPFGLMLVIVTYLQHVDDVAEYVYADEWSFVGGVQ	770	800	830	860	890	920
		270	280	290	300	310	320
SDD17.pep	SVDRSYGAFVNLSHHI-GTHQVHLEPLIIPHYKLNEATKFAAAYPHLVRRNDEPIITA						
CELEFAT	TIDRYLGLDITIMHHITDGHVAHHFENKIPHYHLIATEGVKKVLEPLSDITQYGKSOV	950	980	1010	1040	1070	1100
		330	340	350			
SDD17.pep	FFKTAHLFVNYGAVPETAQIFTLKESAAAAAKAKSD						
CELEFAT	NYDFFARFLWFNYKLDYLVHKTAGIMQFRTILEEKAKAKGKNIPCRSRVQQQLLRPHRPF	1130	1160	1190	1220	1250	1280

Figure 6

Gene Sequence of *sdd12*, a Delta 12-Desaturase Gene
from *Saprolegnia diclina* (ATCC 56851)

1 ATGTGCAAAG GTCAAGCTCC TTCCAAGGCC GACGTGTTC ACCTGCGGG
51 GTACCGCCCG GTCGCGGCA CGCCGAGCC GCTGCGCTG GAGCCCCGA
101 CGATCACGCT CAAGGACCTG CGCGCGGCGA TCCCGGCCCA CTGCTTTGAG
151 CGCAGCGCTG CCACTAGCTT TTACCATTTG GCAGAAGCC TTGCGATCTG
201 CGCGGCGGTG TTCGCGTTG GCCTCAAGCT CGCGGCTGCC GACTTGCCGC
251 TCGCGGCCAA GCTGGTCGCG TGGCCATCT ACTGTTTCGT CCAGGGCACG
301 TACTTTACGG GCATCTGGGT CATTGCGCAC GAATGCGGCC ACCAGGCGTT
351 CTCGGCGTCC GAGATCCTCA ACGACACGGT CGGTATCATT CTTCACTCGC
401 TCCTCTTTGT GCCGTACCAC AGCTGGAAGA TCACGCACCG CCGCCACCAC
451 TCCAACACGG GCAGCTCGCA GAACGACGAG GTGTTTACG CGACGCCCGG
501 GTCCGTCGTC GAGGCCAAGC ACGACCACTC GCTCCTCGAA GAGAGCCCGC
551 TCTACAACCT GTACGGCATC GTCATGATGC TTTCGTGGG CTGGATGCCG
601 GGCTACCTCT TCTTCAACGC GACCGGCCCG ACCAAGTACG CTGGCCTCGC
651 CAAGTCGCAC TTCAACCCGT ACGCAGCCTT TTTCTCCCA AAGGAGCGCC
701 TCAGCATCTG GTGGAGCGAC CTCTGCTTCC TCGCGGCCTT GTACGGCTTT
751 GGCTACGCG TCTCGGTCTT CGGCCTCCTC GATGTCGCC GCCACTACAT
801 CGTGCCGTAC CTCATTTGCA ACGCGTACCT CGTGCTCATC ACGTACCTCC
851 AGCACACGGA TACGTACGTG CCCCCTTCC GCGCGACGA GTGGAAGTGG
901 CTGCGCGGCG CGCTCTGCAC CGTCGACCGC TCGTTCGGCG CGTGGATCGA
951 CAGCGCGATC CACCACATTG CCGACACGCA CGTGACGCAC CACATTTTCT
1001 CCAAGACGCC CTTCTACCAC GCGATCGAGG CGACCGACGC CATCAGCCCC
1051 CTCCTCGGCA AGTACTACCT CATCGACCCG ACGCGATCC CGTGCGCGCT
1101 CTGGCGCTCG TTCACGCACT GCAAGTACGT CGAGGACGAC GGCACGTTG
1151 TGTTTACAA GCGCAAGCTC GAGGAAAAGT AA

Figure 7

Amino Acid Sequence of a Delta 12-Desaturase (SDD12) from *Saprolegnia diclina* (ATCC 56851)

1 MCKGQAPSKA DVFHAAGYRP VAGTPEPLPL EPPTITLKDL RAAIPAHCFE
51 RSAATSFYHL AKNLAICAGV FAVGLKLAAA DLPLAAKLVA WPIYWFVQGT
101 YFTGIWVIAH ECGHQAFSAS EILNDTVGII LHSLLFVPYH SWKITHRRHH
151 SNTGSCENDE VFTPTPRSVV EAKHDHSILLE ESPLYNLYGI VMMLLVGWMP
201 GYLFFNATGP TKYAGLAKSH FNPYAFFLP KERLSIWWSL LCFLAALYGF
251 GYGVSFVGLL DVARHYIVPY LICNAYLVLI TYLQHTDTYV PHFRGDEWNW
301 LRGALCTVDR SFGAWIDSAI HHIADTHVTH HIFSKTPPYH AIEATDAITP
351 LLGKYYLIDP TPIPLALWRS FTHCKYVEDD GNVVIFYRKL EEK*

Figure 8

Comparative analysis of *S. diclina* Delta 12-desaturase (SDD12.pep)
& *G. hirsutum* Delta 12-desaturase (GHO6DES)

Frame: 3 initn: 992 init1: 413 opt: 1086 2-score: 1531.8 expect(): 2.3e-77
45.6% identity in 379 aa overlap
(9-380:14-384)

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SDD12.pep      10      20      30      40
                MCKGQAPSKADVPHAAGYRFVAGTPEP-----LPLEPPITITLKDRAATPAHC
                ||: : |:| |:| | | : |:| | :| :| :| || ||
GHO6DESAT      10      40      70      100     130     160
                LRVSSITWRXTAFPKASKMGAGGRMPIDGLKEENRGSVNRVPIETKPPFTLGQIKQATPPHC

SDD12.pep      50      60      70      80      90     100
                FERSAATSFYHLAKNLAICAGVFAVGLKLAADLEPLAAKLVA MPIYWEVQGYTFGIWVI
                |:| | | : : :| : : : :| | : :| |:| | :| :| :| :|
GHO6DESAT      190     220     250     280     310     340
                FRSLRLRSFSYVVHDLCLASFPPYIATSYFHF-LPPQFSYIAWPVYVWLQGCILITGVWVI

SDD12.pep      110     120     130     140     150     160
                AHEGQHQAFSASEITNDIVGIIILHSLLFVPHYSMKLTTHRRHNSNGSCENDEVPTPTPRS
                :|:| :| : :| :| :| :| :| :| :| :| :| :| :| :| :| :|
GHO6DESAT      370     400     430     460     490     520
                AHEWGHHAFRDYQWDDTVGLILHSALLVPYFSWKLSHRRHNSNGSMERDEVVPKPKS

SDD12.pep      170     180     190     200     210     220
                VVEAKHDHSLLESPLYNLYGIVMMLLVGAMPGYLFENATGPKFYAGLAKSHFNPYAAFF
                : : : :| : :| :| :| :| :| :| :| :| :| :| :| :| :|
GHO6DESAT      550     580     610     640     670
                KLSC---FAKYLNNPPGRVLSLVVLTITLGM-PMYLAFNVSG---RYYDRILASHYNPYGPIY

SDD12.pep      230     240     250     260     270     280
                LPKERLSIWMSDLCLFAALYGFQGVSVFGLLDVARHYIVPYLIGNAYLVLLITLYLQHTDT
                :|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
GHO6DESAT      700     730     760     790     820     850
                SDRERLQVYISDTIGIFAVTYVLYKIAATKGLAWLLCTYGVPLLVNAFVLLITLYLQHTS

SDD12.pep      290     300     310     320     330     340
                YVYFRGDEANMLRGALCTVDRSPGAWIDSAIHTIADTHVTHIFSKTIPFYHATFATDAI
                :|:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
GHO6DESAT      880     910     940     970     1000    1030
                ALPHYDSSENDMLRGALSTMDRFGV-LNKVFHNITDTHVAHLFTSMFYHAMEATKAI

SDD12.pep      350     360     370     380     390
                TPLLKYYLLDPTPIPLALWRSFTHCYKVEDDGNVVFYRKLLEEK
                |:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
GHO6DESAT      1060    1090    1120    1150    1180    1210
                KPILKGYYPFDGTPITYKAMNREAKECLYVEPDVGGGGGSGKGVFWYRNKFXRPTNCLTAG

GHO6DESAT      1240    1270    1300    1330    1360
                RRNRKTYLLDXCLGLKLIINRKMNSCLAVLCIKOCINKLYGRKKKK

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116673-01600

Figure 9

Sequence ID:

Sequence ID 1

5'-ATC CGC GCC GCC ATC CCC AAG CAC TGC TGG GTC AAG-3'

Sequence ID 2

5'- GCC CTC TTC GTC CTC GGC CAY GAC TGC GGC CAY GGC TCG TTC TCG-
3'

Sequence ID 3

5'-GAG RTG GTA RTG GGG GAT CTG GGG GAA GAR RTG RTG GRY GAC RTG-3'

Sequence ID 4

5'-CCC TAC CAY GGC TGG CGC ATC TCG CAY CGC ACC CAY CAY CAG AAC-3'

Sequence ID 5

5'-GTT CTG RTG RTG GGT CCG RTG CGA GAT GCG CCA GCC RTG GTA GGG-3'

Sequence ID 6

5'- GGC TCG CAC TTC SAC CCC KAC TCG GAC CTC TTC GTC-3'

Sequence ID 7

5'- GAC GAA GAG GTC CGA GTM GGG GTW GAA GTG CGA GCC-3'

Sequence ID 8

5'- GCG CTG GAK GGT GGT GAG GCC GCC GCG GAW GSA CGA CCA-3'

Sequence ID 9

5'- CTG GGG GAA GAG RTG RTG GAT GAC RTG GGT GCC GAT GTC RTG RTG-
3'

Sequence ID 10

5'- GGT GGC CTC GAY GAG RTG GTA RTG GGG GAT CTK GGG GAA GAR RTG-
3'

Sequence ID 11

5'-GAG RTG GTA RTG GGG GAT CTG GGG GAA GAR RTG RTG GRY GAC RTG-3'

Sequence ID 12

5'-TAC GCG TAC CTC ACG TAC TCG CTC G-3'

Sequence ID 13

5'-TTC TTG CAC CAC AAC GAC GAA GCG ACG-3'

Sequence ID 14

5'-GGA GTG GAC GTA CGT CAA GGG CAA C-3'

Sequence ID 15

5'-TCA AGG GCA ACC TCT CGA GCG TCG AC-3'

Sequence ID 16

5'-CCC AGT CAC GAC GTT GTA AAA CGA CGG CCA G-3'

Sequence ID 17

5'- AGC GGA TAA CAA TTT CAC ACA GGA AAC AGC -3'

Sequence ID 18

5'-GGT AAA AGA TCT CGT CCT TGT CGA TGT TGC-3'

Sequence ID 19

5'-GTC AAA GTG GCT CAT CGT GC-3'

Sequence ID 20

5'-CGA GCG AGT ACG TGA GGT ACG CGT AC-3'

Sequence ID 21

5'-TCA ACA GAA TTC ATG ACC GAG GAT AAG ACG AAG GTC GAG TTC CCG-3'

Sequence ID 22

5'-AAA AGA AAG CTT CGC TTC CTA GTC TTA GTC CGA CTT GGC CTT GGC-3'

Sequence ID 23

5'-TCA ACA AAG CTT ATG ACC GAG GAT AAG ACG AAG GTC GAG TTC
CCG-3'

Sequence ID 24

5'-AAA AGA GAA TTC CGC TTC CTA GTC TTA GTC CGA CTT GGC CTT
GGC-3'

Sequence ID 25

1 ATGACTGAGG ATAAGACGAA GGTGAGTTC CCGACGCTCA CGGAGCTCAA
51 GCACTCGATC CCGAACGCGT GCTTTGAGTC GAACCTCGGC CTCTCGCTCT
101 ACTACACGGC CCGCGCGATC TTCAACGCGT CGGCCTCGGC GCGCTGCTC
151 TACGCGGCGC GCTCGACGCC GTTCATTGCC GATAACGTTC TGCTCCACGC
201 GCTCGTTTGC GCCACCTACA TCTACGTGCA GGGCGTCATC TTCTGGGGCT
251 TCTTCACGGT CGGCCACGAC TGGCGCCACT CGGCCTTCTC GCGTACCAC
301 AGCGTCAACT TTATCATCGG CTGCATCATG CACTCTGCGA TTTTGACGCC
351 GTTCGAGAGC TGGCGCGTGA CGCACCGCCA CCACCACAAG AACACGGGCA
401 ACATTGATAA GGACGAGATC TTTTACCCGC ACCGGTCGGT CAAGGACCTC
451 CAGGACGTGC GCCAATGGGT CTACACGCTC GCGGTGCGT GGTTTGTCTA
501 CTTGAAGTTC GGGTATGCC CGCGCACGAT GAGCCACTTT GACCCGTGGG
551 ACCCGCTCCT CCTTCGCCGC GCGTCGGCGC TCATCGTGTC GCTCGGCGTC
601 TGGGCGCGCT TCTTCGCCGC GTACGCGTAC CTCACATACT CGCTCGGCTT
651 TGCCGTCATG GGCCTCTACT ACTATGCGCC GCTCTTTGTC TTTGCTTCGT
701 TCCTCGTCAT TACGACCTTC TTGCACCACA ACGACGAAGC GACGCGTGG
751 TACGGCGACT CGGAGTGGAC GTACGTCAAG GGCAACCTCT CGAGCGTCGA
801 CCGCTCGTAC GCGCGGTTTC TGGACAACT GAGCCACCAC ATTGGCACGC
851 ACCAGGTCCA CCATTGTGTC CCGATCATTC CGCACTACAA GCTCAACGAA
901 GCCACCAAGC ACTTTGCGGC CGCGTACCCG CACCTCGTGC GCAGGAACGA
951 CGAGCCCATC ATCACGGCCT TCTTCAAGAC CGCGCACCTC TTTGTCAACT
1001 ACGGCGCTGT GCCCGAGACG GCGCAGATCT TCACGCTCAA AGAGTCGGCC
1051 GCGGCGGCCA AGGCCAAGTC GGACTAA

Sequence ID 26

1 MTEDKTKVEF PTLTELKHSI PNACFESNLG LSLYYTARAI FNASASAALL
 51 YAARSTPFIA DNVLLHALVC ATYIYVQGI FWGFFTVGHD CGHSAFSRYH
 101 SVNFIIGCIM HSAILTPFES WRVTHRHHHK NTGNIDKDEI FYPHRSVKDL
 151 QDVRQWVYTL GGAWFVYLKV GYAPRTMSHF DPWDPLLLRR ASAVIVSLGV
 201 WAAFFAAYAY LTYSLGFAM GLYYYAPLFV FASFLVITTF LHHNDEATPW
 251 YGDSEWTYVK GNLSSVDRSY GAFVDNLSSH IGTHQVHHLF PIIPHYKLINE
 301 ATKHFAAAYP HLVRNDEPI ITAFFKTAHL FVNYGAVPET AQIFTLKESA
 351 AAAKAKSD*

Sequence ID 27

1 ATGGCCCCGC AGACGGAGCT CCGCCAGCGC CACGCCGCCG TCGCCGAGAC
 51 GCCGGTGGCC GGCAAGAAGG CCTTTACATG GCAGGAGTGC GCGCAGCACA
 101 ACACGGCGCG CTCGGCCTGG ATCATTATCC GCGGCAAGGT CTACGACGTG
 151 ACCGAGTGGG CCAACAAGCA CCCC GGCGCG CGCGAGATGG TGCTGCTGCA
 201 CGCCGGTTCG GAGGCCACCG ACACGTTTCA CTCTGACCAC CCGTTCAGCG
 251 ACAAGGCCGA GTCGATCTTG AACAAAGTATG AGATTGGCAC GTTCACGGGC
 301 CCGTCCGAGT TTCCGACCTT CAAGCCGGAC ACGGGCTTCT ACAAGGAGTG
 351 CCGCAAGCGC GTTGGCGAGT ACTTCAAGAA GAACAACCTC CATCCGACGG
 401 ACGGCTTCCC GGGCCTCTGG CGCATGATGG TCGTGTTTGC GGTGCGCCGGC
 451 CTCGCTTGTG ACGGCATGCA CTTTTCGACT ATCTTTGCGC TGCAGCTCGC
 501 GGCCGCGGCG CTCTTTGGCG TCTGCCAGGC GCTGCCGCTG CTCCACGTCA
 551 TGCACGACTC GTCGCACGCG TCGTACACCA ACATGCCGTT CTTCATTAC
 601 GTCGTCGGCC GCTTTGCCAT GGAAGTGTTC GCCGGCGGCT CGATGGTGTG
 651 ATGGCTCAAC CAGCACGTGC TGGGCCACCA CATCTACAG AACGTCGCGG
 701 GCTCGGACCC GGATCTTCCG GTCAACATGG ACGGCGACAT CCGCCGCATC
 751 GTGAACCGCC AGGTGTTCGA GCCCATGTAC GCATTCCAGC ACATCTACCT
 801 TCCGCGGCTC TATGGCGTGC TTGGCCTCAA GTTCCGCATC CAGGACTTCA
 851 CCGACACGTT CGGCTCGCAC ACGAACGGCC CGATCCGCGT CAACCCGCAC
 901 GCGCTCTCGA CGTGGATGGC CATGATCAGC TCCAAGTCGT TCTGGGCCTT
 951 CTACCCGCTG TACCTTCCGC TTGCCGTGCT CCAGATGCCC ATCAAGACGT
 1001 ACCTTGCATC CTCTTCTCTC GCCGAGTTTG TCACGGGCTG GTACCTCGCG
 1051 TTCAACTTCC AAGTAAGCCA TGTCTCGACC GAGTGGCGCT ACCCATGCGG
 1101 CGACGAGGCC AAGATGGCGC TCCAGGACGA GTGGGCAGTC TCGCAGGTCA

1151 AGACGTCGGT CGACTACGCC CATGGCTCGT GGATGACGAC GTTCCTTGCC
 1201 GGC GCGCTCA ACTACCAGGT CGTGCACCAC TTGTTCCTCCA GCGTGTGCGCA
 1251 GTACCACATAC CCGCGCATCG CGCCCATCAT CGTCGACGTC TGCAAGGAGT
 1301 ACAACATCAA GTACGCCATC TTGCCGGACT TTACGGCGGC GTTCGTTGCC
 1351 CACTTGAAGC ACCTCCGCAA CATGGGCCAG CAGGGCATCG CCGCCACGAT
 1401 CCACATGGGC TAA

Sequence ID 28

1 ATGGCAAACA GCAGCGTGTG GGATGATGTG GTGGGCCGCG TGGAGACCGG
 51 CGTGGACCAG TGGATGGATG GCGCCAAGCC GTACGCACCTC ACCGATGGGC
 101 TCCCGATGAT GGACGTGTCC ACCATGCTGG CATTCGAGGT GGGATACATG
 151 GCCATGCTGC TCTTCGGCAT CCCGATCATG AAGCAGATGG AGAAGCCTTT
 201 TGAGCTCAAG ACCATCAAGC TCTTGCAACA CTTGTTTCTC TTCGGACTTT
 251 CCTTGATACAT GTGCGTGGAG ACCATCCGCC AGGCTATCCT CGGAGGCTAC
 301 AAAGTGTTTG GAAACGACAT GGAGAAGGGC AACGAGTCTC ATGCTCAGGG
 351 CATGTCTCGC ATCGTGTACG TGTCTGCGT GTCCAAGGCA TACGAGTTCT
 401 TGGATACGCG CATCATGATC CTTTGCAAGA AGTTCAACCA GGTTCCTTC
 451 TTGCATGTGT ACCACCATGC CACCATTTT GCCATCTGGT GGGCTATCGC
 501 CAAGTACGCT CCAGGAGGTG ATGCGTACTT TTCAGTGATC CTCAACTCTT
 551 TCGTGACAC CGTCATGTAC GCATACTACT TCTTCTCCTC CCAAGGGTTC
 601 GGGTTCGTGA AGCCAATCAA GCCGTACATC ACCACCTTC AGATGACCCA
 651 GTTCATGGCA ATGCTTGTGC AGTCCTTGTA CGACTACCTC TTCCCATGCG
 701 ACTACCACA GGCCTTGTG CAGCTTCTTG GAGTGTACAT GATCACCTTG
 751 CTTGCCCTCT TCGGCAACTT TTTTGTGCAG AGCTATCTTA AAAAGCCAAA
 801 AAAGAGCAAG ACCAACTAA

Sequence ID 29

1 MTVGFDETVT MDTVRNHNMP DDAWCAIHGT VYDITKFSKV HPGGDIIMLA
 51 AGKEATILFE TYHIKGVPA VLRKYKVGKL PQGKKGETSH MPTGLDSASY
 101 YSWDSEFYRV LRERVAKKLA EPLMQRARM ELWAKAIFLL AGFWGSLYAM
 151 CVLDPHGGAM VAAVTLGVFA AFVGTCTIQHD GSHGAFSKSR FMNKAAGWTL
 201 DMIGASAMTW EMQHVLGHHP YTNLIEMENG LAKVKGADVD PKKVDQESDP
 251 DVFSTYPLMR LHPWHRQRFY HKFQHLIYAPL IFGFMTINKV ISQDVGVVLR
 301 KRLFQIDANC RYGSPWNVAR FWIMKLLTTL YMVALPMYMQ GPAQGLKLFF

351 MAHFTCGEVL ATMFIIVNHII EGVSYASKDA VKGVMAPPRT VHGVTPMQVT
401 QKALSAAEST KSDADKTTMI PLNDWAAVQC QTSVNWAVGS WFWNHFSGGL
451 NHQIEHHCFP QNPHTVNVYI SGIVKETCEE YGVPYQAEIS LFSAYFKMLS
501 HLRTLGNEDL TAWST*

Sequence ID 30

5'-CCG SAG TTC ACS ATC AAG GAG ATC CGC GAS KSC ATC CCG GCC
CAC TGC TTC -3'

Sequence ID 31

5'-GRS CTT CTT GAK GTG GWM SGT GGC CTC CTC GGC GTG GTA GWR
CGG CAT-3'

Sequence ID 32

5'-CCS STC TAC TGG GCC TGC CAG GGT RTC GTC CTC ACS GGT GTC
TGG-3'

Sequence ID 33

5'-CCS STC TAC TGG ATC RYS CAG GGT RTC GTC KGY ACS GGT GTC
TGG-3'

Sequence ID 34

5'-GGC GTG GTA GTG CGG CAT SMM CGA GAA GAR GTG GTG GGC GAC
GTG-3'

Sequence ID 35

5'-CAC GTA CCT CCA GCA CAC GGA CAC CTA CG-3'

Sequence ID 36

5'- GAT CGA CAG CGC GAT CCA CCA CAT TGC-3'

Sequence ID 37

5'- CAA ATG GTA AAA GCT AGT GGC AGC GCT GC-3'

Sequence ID 38

5'-AGT ACG TGC CCT GGA CGA ACC AGT AGA TG-3'

Sequence ID 39

5' - TCA ACA GAA TTC ATG TGC AAA GGT CAA GCT CCT TCC AAG GCC
GAC GTG -3'

Sequence ID 40

5' - AAA AGA AAG CTT TTA CTT TTC CTC GAG CTT GCG CTT GTA AAA
CAC AAC-3'

Sequence ID 41

1 ATGTGCAAG GTCAAGCTCC TTCCAAGGCC GACGTGTTCC ACGCTGCGGG
51 GTACCGCCCG GTCGCGGCA CGCCCGAGCC GCTGCCGCTG GAGCCCCGCA
101 CGATCACGCT CAAGGACCTG CGCGCGGCGA TCCCGGCCCA CTGCTTTGAG
151 CGCAGCGCTG CCACTAGCTT TTACCATTTG GCCAAGAACC TTGCGATCTG
201 CGCCGCGCTG TTCGCCGTTG GCCTCAAGCT CGCGGCTGCC GACTTGCCGC
251 TCGCGGCCAA GCTGTCGCG TGGCCCATCT ACTGGTTGCT CCAGGGCAG
301 TACTTTACGG GCATCTGGGT CATTGCGCAC GAATGCGGCC ACCAGGCGTT
351 CTCGGCGTCC GAGATCCTCA ACGACACGGT CGGTATCATT CTTCACTCGC
401 TCCTCTTTGT GCCGTACCAC AGCTGGAAGA TCACGCACCG CCGCCACCAC
451 TCCAACACGG GCAGCTGCGA GAACGACGAG GTGTTTACGC CGAGCCGCG
501 GTCGTCGCTC GAGGCCAAGC ACGACCACTC GCTCCTCGAA GAGAGCCCGC
551 TCTACAACCT GTACGGCATC GTCATGATGC TTCTCGTGGG CTGGATGCCG
601 GGCTACCTCT TCTTCAACGC GACCGGCCCG ACCAAGTACG CTGGCCTCGC
651 CAAGTCGCAC TTCAACCCGT ACGCAGCCTT TTCTCTCCCA AAGGAGCGCC
701 TCAGCATCTG GTGGAGCGAC CTCTGCTTCC TCGCGGCCTT GTACGGCTTT
751 GGCTACGGCG TCTCGGTCTT CGGCCTCCTC GATGTCGCCC GCCACTACAT
801 CGTGCCGTAC CTCAATTGCA ACGCGTACCT CGTGCTCATC ACGTACCTCC
851 AGCACACGGA TACGTACGTG CCCCCTTCC GCGGCGACGA GTGGAACGG
901 CTGCGCGGCG CGCTCTGCAC CGTCGACCGC TCGTTCGGCG CGTGGATCGA
951 CAGCGCGATC CACCACATG CCGACACGA CGTGACGCAC CACATTTTCT
1001 CCAAGACGCC CTCTTACCAC GCGATCGAGG CGACCGACGC CATCACGCC
1051 CTCCTCGGCA AGTACTACCT CATCGACCG ACGCCGATCC CGCTGGCGCT
1101 CTGGCGCTCG TTCACGCACT GCAAGTACGT CGAGGACGAC GGCAACGTTG

1151 TGTITTACAA GCGCAAGCTC GAGGAAAAGT AA

Sequence ID 42

1 MCKGQAPSKA DVFHAAGYRP VAGTPEPLPL EPPTITLKDL RAAIPAHCFE
51 RSAATSFYHL AKNLAICAGV FAVGLKLAAA DLPLAAKLVA WPIYWFVQGT
101 YFTGIWVIAH ECGHQAFSAS EILNDTVGII LHSLLFVPYH SWKITHRRHH
151 SNTGSCENDE VFTPTPRSVV EAKHDHSLLE ESPLYNLYGI VMMLLVGWMP
201 GYLFFNATGP TKYAGLAKSH FNPYAAFFLP KERLSIWWSL LCFLAALYGF
251 GYGVSVFGLL DVARHYIVPY LICNAYLVLI TYLQHTDTYV PHFRGDEWNW
301 LRGALECTVDR SFGAWIDSAI HHIADTHVTH HIFSKTPFYH AIEATDAITP
351 LLGKYYLIDP TPIPLALWRS FTHCKYVEDD GNVVFYKRKL EEK*